

Fig 1

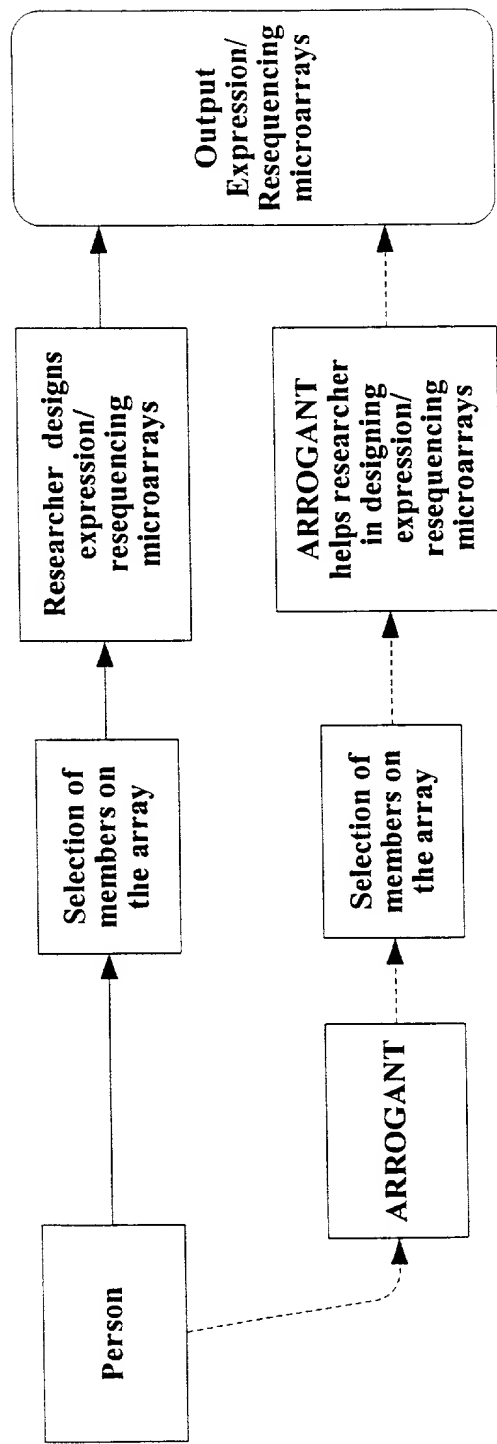


Fig 2

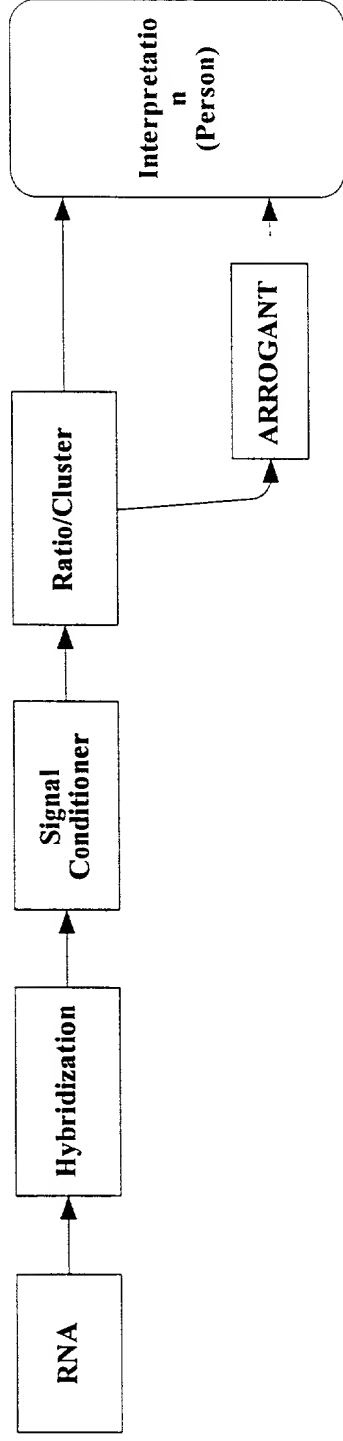


Fig 3

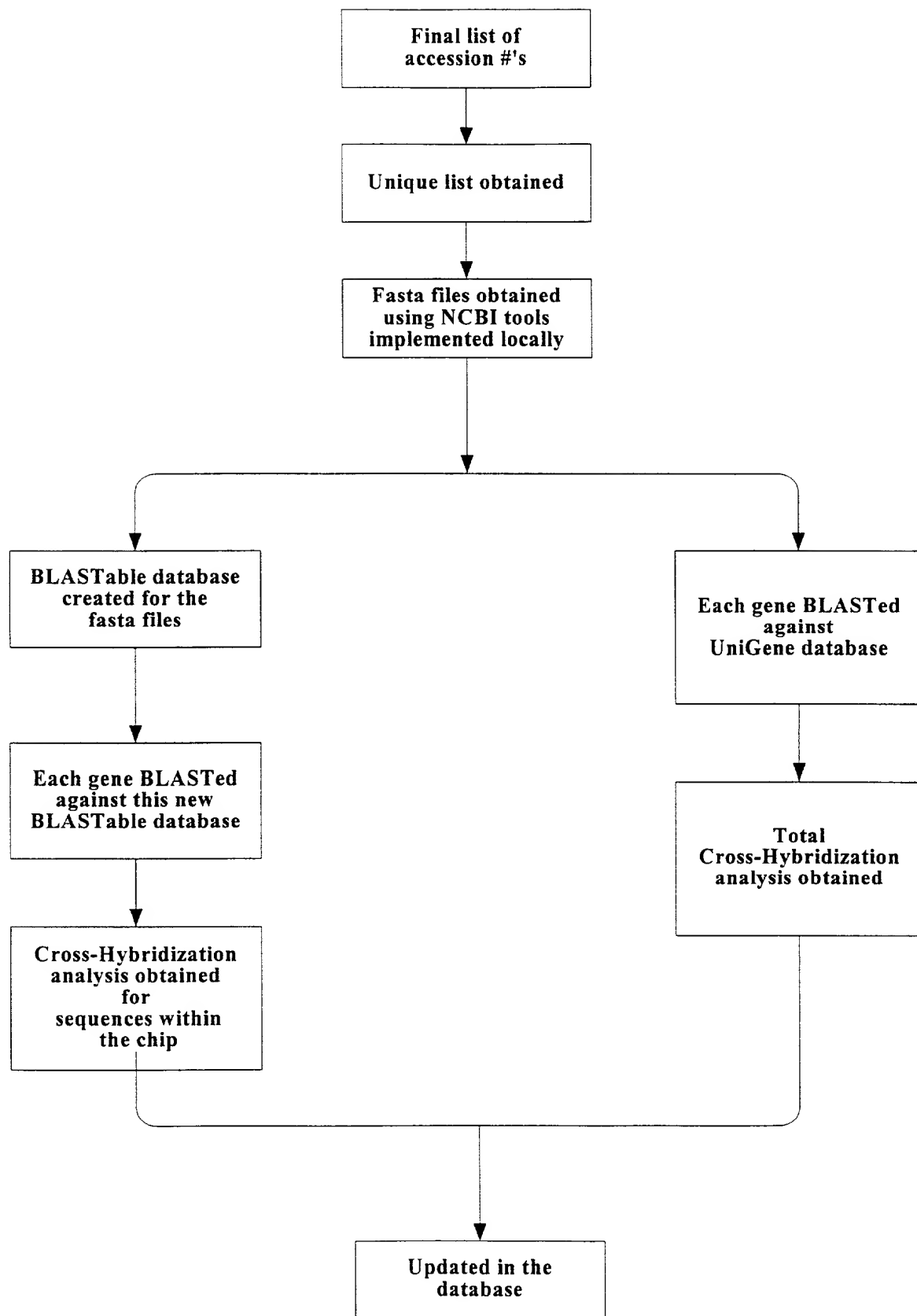


Fig 4

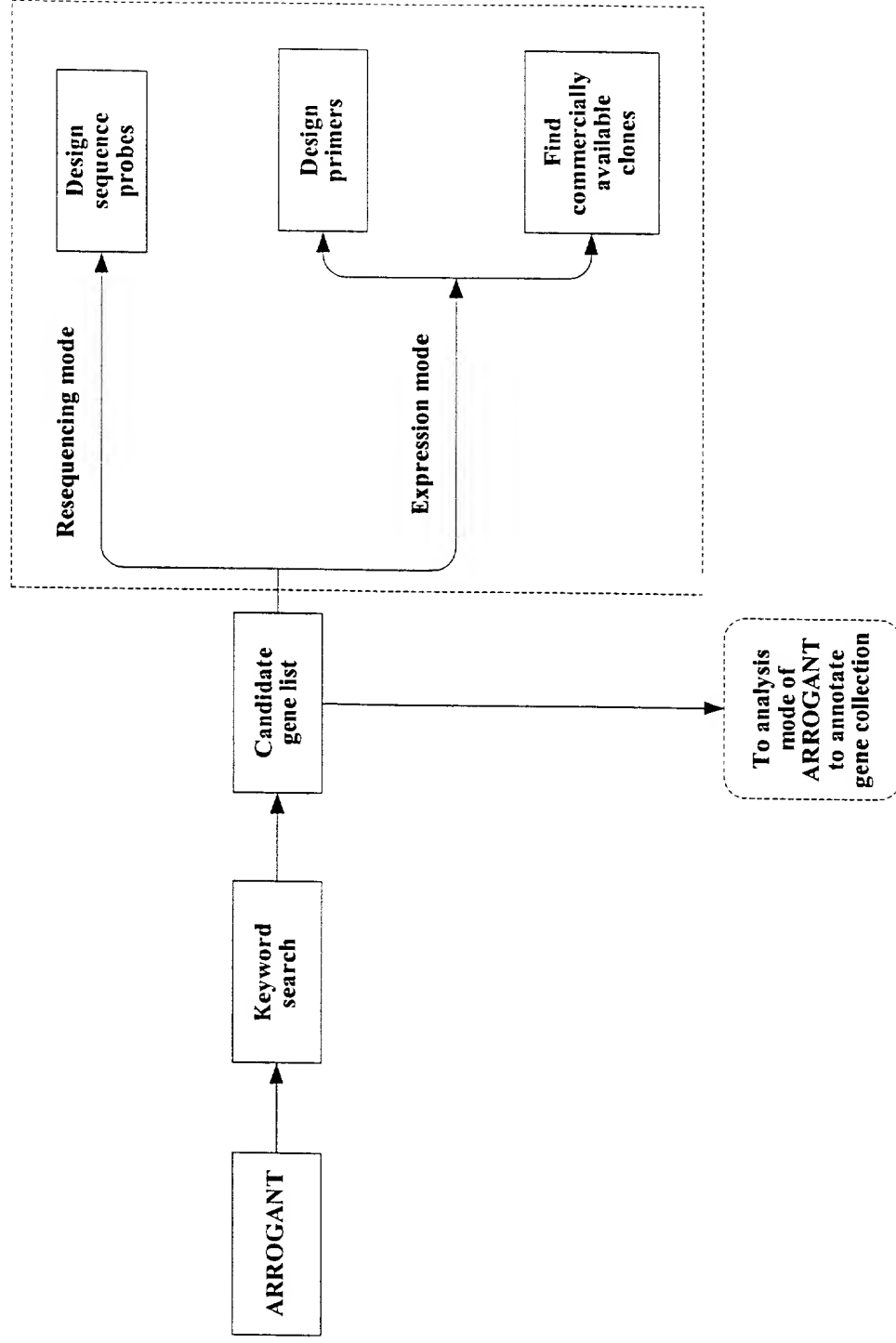


Fig 5

ArrayGene: Array Organizing Tool - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Refresh Home Search Favorites History Mail Edit Print

Links My Links My Recent My Favorites My History My Favorites My History My Favorites My History

Address: http://manager.sswmed.edu/myweb/index.asp

click on Species

User Email: jalkw01@sswmed.edu

Array Name: jga

Number of Array Members: 110 Use: r Resequencing r Expression

Source: r PCR Products r Clones r Both r 3' Exon End Only r Random Exons

Keywords: cardiac hypertrophy

Databases: r GenBank r UniGene r LocusLink r KEGG r KEGG Pathway r Research Genetics

Status: 26/12/01 10:36:36 AM 11/11/01

Fig 6

Fig 7

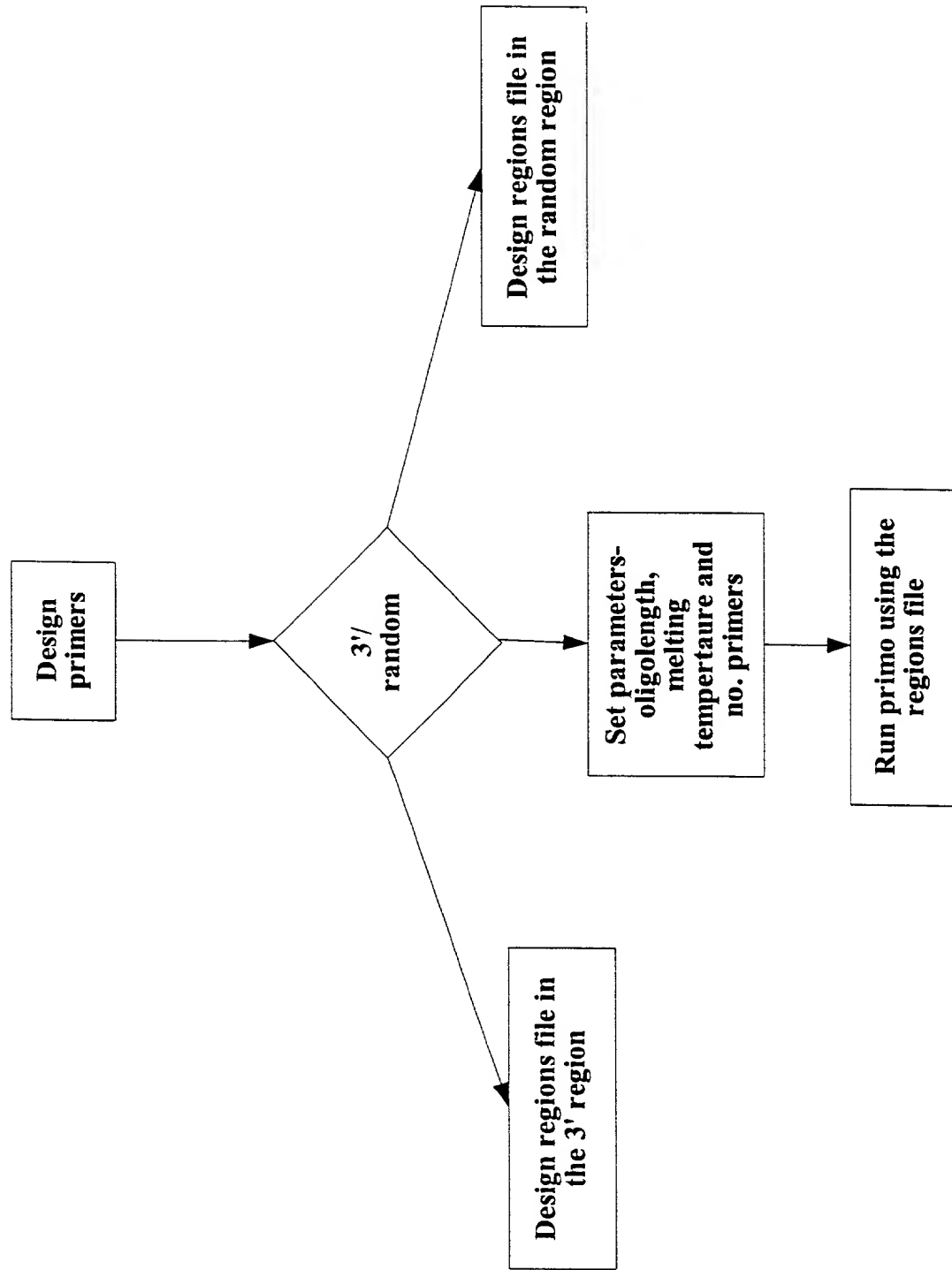


Fig 8

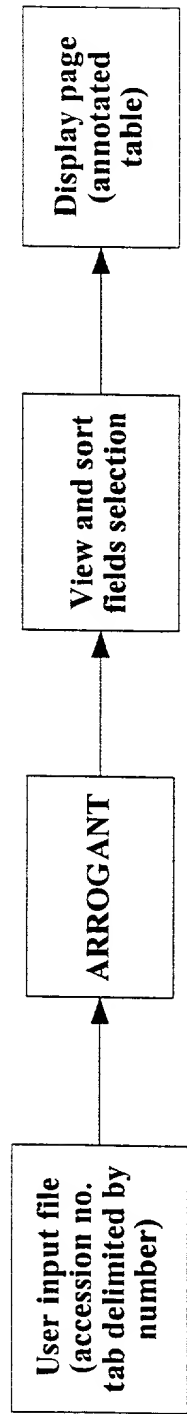


Fig 9

Select the fields you want to view, select how you would like to sort the data and press

Show Collection

<input type="checkbox"/> Accession	<input type="checkbox"/> IMAGE identifier	<input type="checkbox"/> Alias protein
<input type="checkbox"/> Expression level data	<input type="checkbox"/> Xhyb analysis	<input type="checkbox"/> Phenotype
<input type="checkbox"/> Unique identifier	<input type="checkbox"/> Tissues	<input type="checkbox"/> Phenotype ID/ OMIM ID
<input type="checkbox"/> Title	<input type="checkbox"/> GDB	<input type="checkbox"/> Chromosome
<input type="checkbox"/> PubMed	<input type="checkbox"/> Gene name	<input type="checkbox"/> Map location
<input type="checkbox"/> Related Proteins	<input type="checkbox"/> Gene Function	<input type="checkbox"/> Map link
<input type="checkbox"/> Related Sequences	<input type="checkbox"/> Synonyms	<input type="checkbox"/> Map type
<input type="checkbox"/> Taxonomy	<input type="checkbox"/> Pathway	<input type="checkbox"/> STS- marker name
<input type="checkbox"/> Repeats	<input type="checkbox"/> SNP analysis	<input type="checkbox"/> STS- chromosome
<input type="checkbox"/> Hairpin/Palindrome	<input type="checkbox"/> Unigene ID	<input type="checkbox"/> STS- ID
<input type="checkbox"/> Homology	<input type="checkbox"/> Locus ID	<input type="checkbox"/> Reviewed RefSeq
<input type="checkbox"/> Research Genetics Clone	<input type="checkbox"/> Alias symbol	<input type="checkbox"/> cDNA Source

Sort Preferences

1.
2.
3.
4.
5.

Fig 10

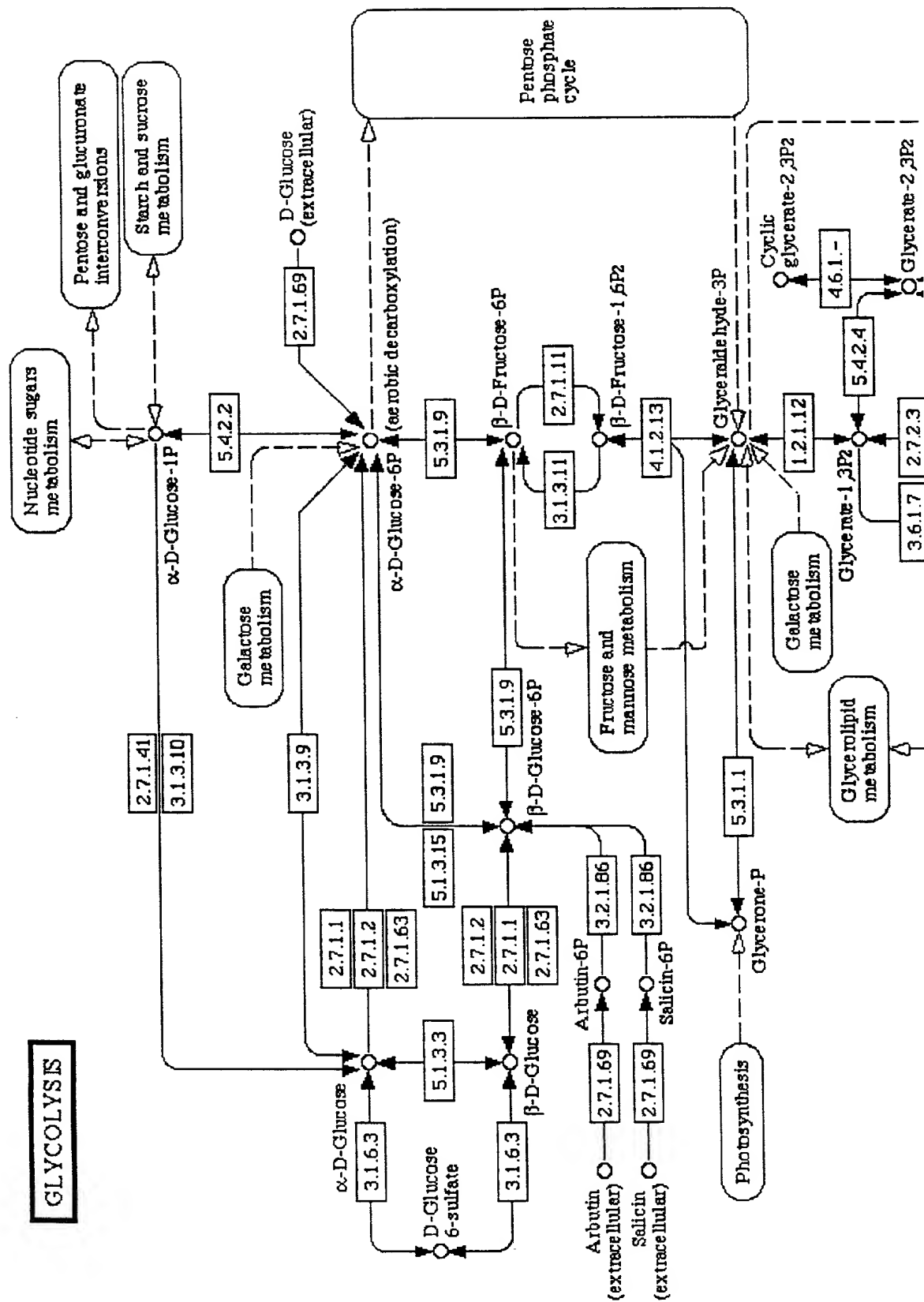
For more information on any input data field click on that link. For example, for help on Accession click on [Accession](#)

Database	Genbank	Pomposus	Locuslink	Unigene	Research Genetics
Last Updated	2/7/01 8:06:55 AM	1/18/01 8:35:24 AM	2/6/01 8:34:29 AM	1/28/01 8:34:45 AM	1/8/01 8:35:59 AM

Results Table

Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function
1	NM_000236	455772	Hs_9994	Homo sapiens lipase, hepatic (LIPC), mRNA.	Mm.362. Rn.1195.	Summary: LIPC encodes hepatic triglyceride lipase which is expressed in liver. LIPC has dual functions of triglyceride hydrolase and ligand, bridging factor for receptor mediated lipoprotein uptake
2	NM_000023	4506910	Hs_99931	Homo sapiens sarcoglycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA.	Mm.18709. Rn.23558.	
Summary	239	232	207	232	201	239
Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function

Fig 11



Column Name	Datatype	Length	Precision	Scale	Allow Null	Default Value
accsno	varchar	9	0	0		((-1))
nid	varchar	10	0	0	✓	((-1))
defn	varchar	255	0	0	✓	((-1))
type	varchar	100	0	0	✓	((-1))
dna	varchar	6	0	0	✓	((-1))
organism	varchar	25	0	0	✓	((-1))
source	varchar	25	0	0	✓	((-1))
keyword	varchar	6	0	0	✓	((-1))
comments	varchar	255	0	0	✓	((-1))
featstuff	varchar	1400	0	0	✓	((-1))
fstart	varchar	10	0	0	✓	((-1))
fend	varchar	10	0	0	✓	((-1))
species	varchar	200	0	0	✓	((-1))
authors	varchar	255	0	0	✓	((-1))
journal	varchar	255	0	0	✓	((-1))
version	varchar	30	0	0	✓	((-1))
reference	varchar	25	0	0	✓	((-1))
title	varchar	100	0	0	✓	((-1))
basepair	varchar	10	0	0	✓	((-1))

Fig 13

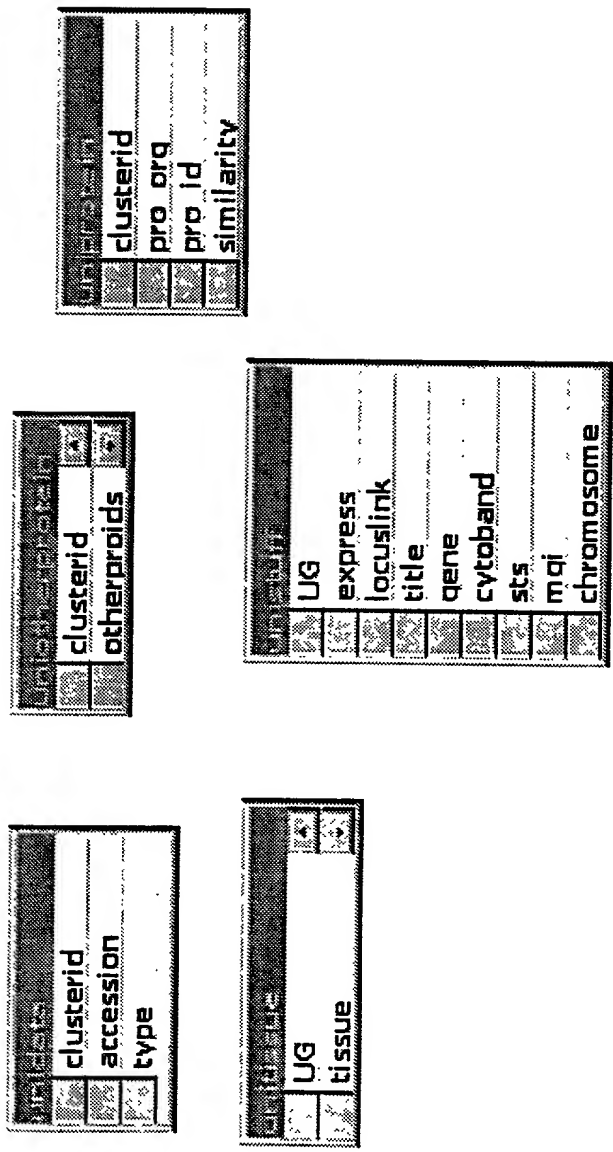


Fig 14

kegg	
	Uniqueld
	Locusid
	Organism
	Name
	Defn
	class
	position
	gdb
	ncbi

lookpath	
	pathno
	pathway

pathway	
	Uniqueld
	pathno
	organism

Fig 16

homoortho	
	Unigid1
	Unigid2
	Locid1
	Locid2
	Acc1
	Acc2

Fig 17























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	[RG Plate]
	[RG row]
	[RG column]
	[Insert Size*]
	[Cluster ID]
	[UG build]
	[Clone ID]
	Vector
	Tissue
	Library
	Accession
	NID
	[Gene Name]
	[Gene Symbol]
	Chromosome
	Band
	Markers
	Col019
	Barcode
	Antibiotics
	[repeat ?]

Fig 18

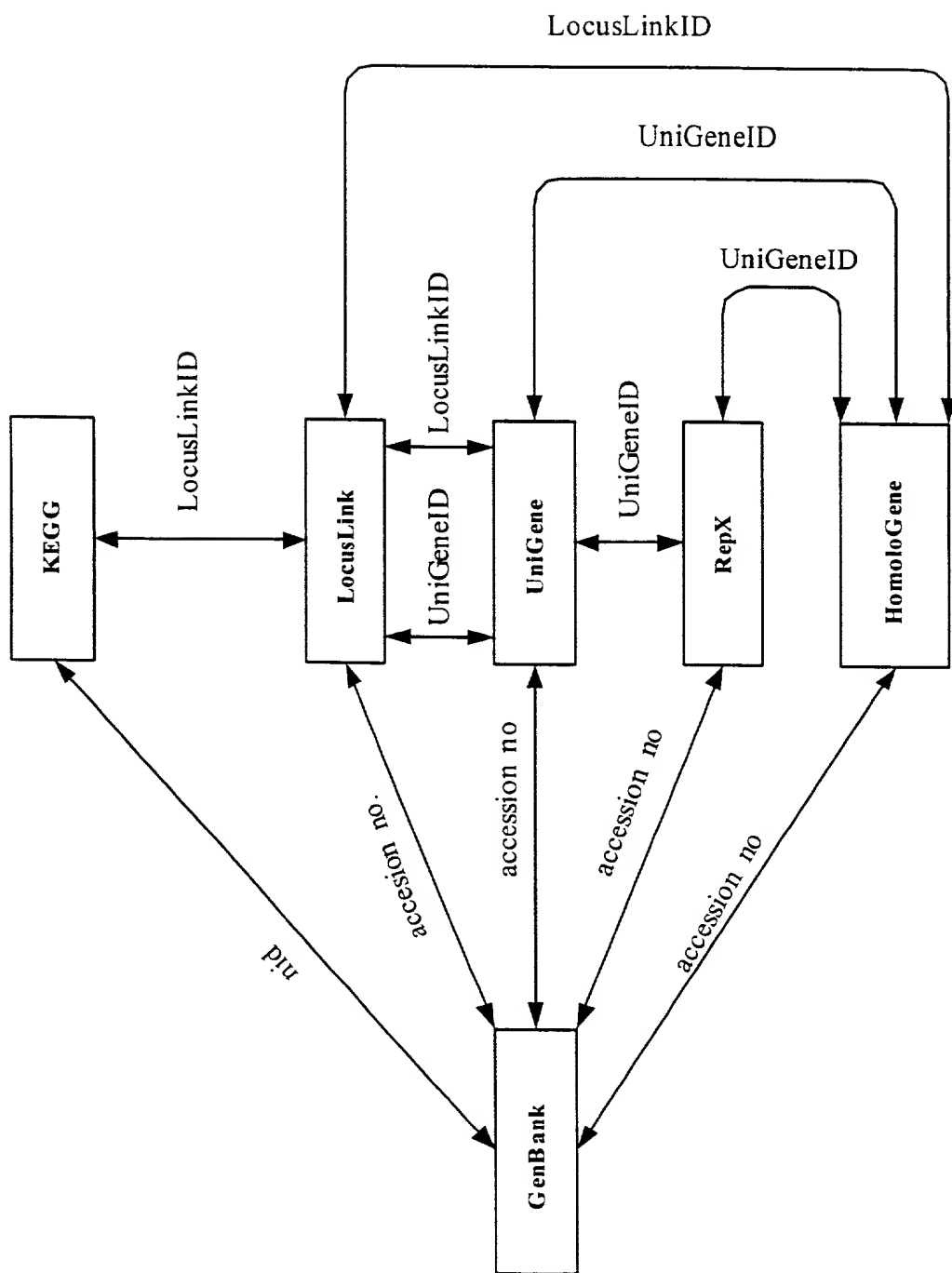


Fig 19

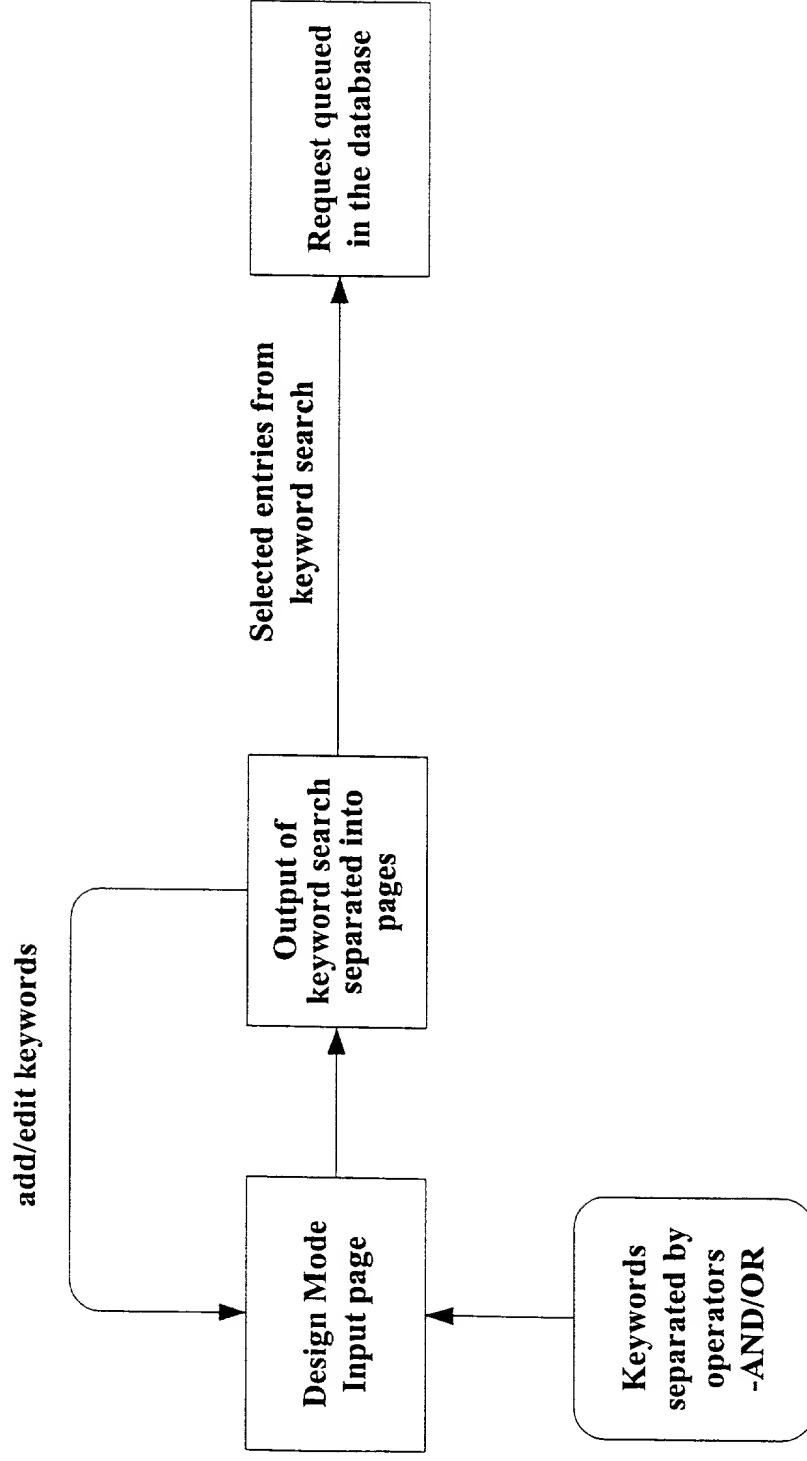


Fig 20

Program runs at regular intervals to process pending requests in the queue

Final List transferred to HP-Unix Super Computer (Chaos)

List sorted and unique list obtained (duplications avoided)

NCBI tools (implemented locally) used to obtain fasta files

Expression

Regions file created either in 3'/random region

Run PRIMO with following parameters (-noequal-all-read)

Primers log fasta files transferred back to database server

Run query to obtain list of clones if required

Resequencing

Convert fasta file to DOC code format

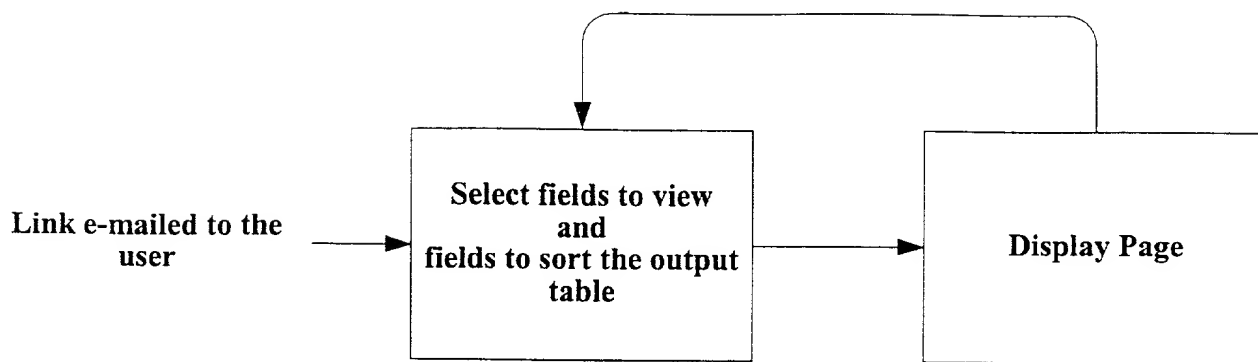
To DOC code

Probes file created

Output files e-mailed to the user

Fig 21





Program runs after regular intervals to process requests in the queue

Run stored procedure 'testcode'

'testcode' annotates each sequence with different items of information and stores it in the database

Cross-Hybridization analysis

Create a link using 'taskID' and e-mail it to the user

Fig 22

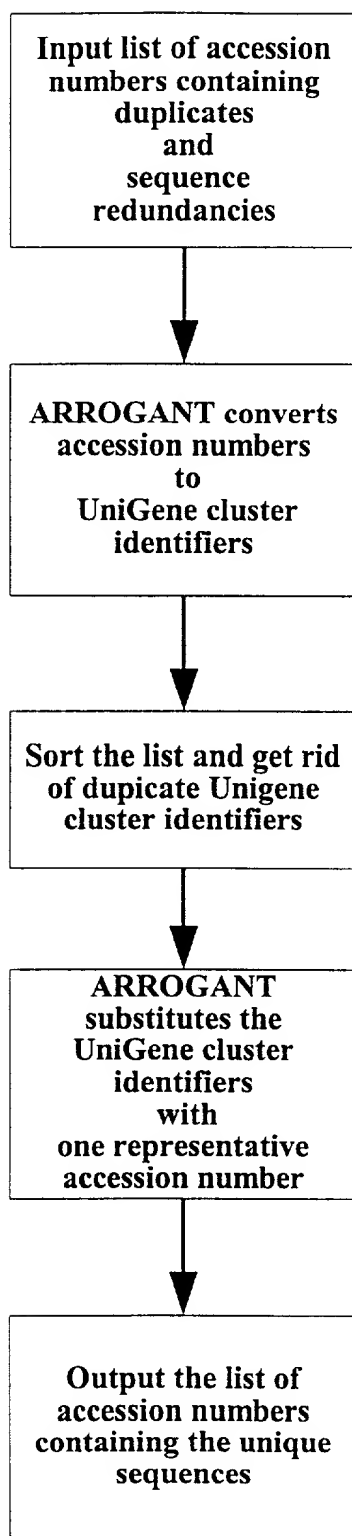


Fig 23

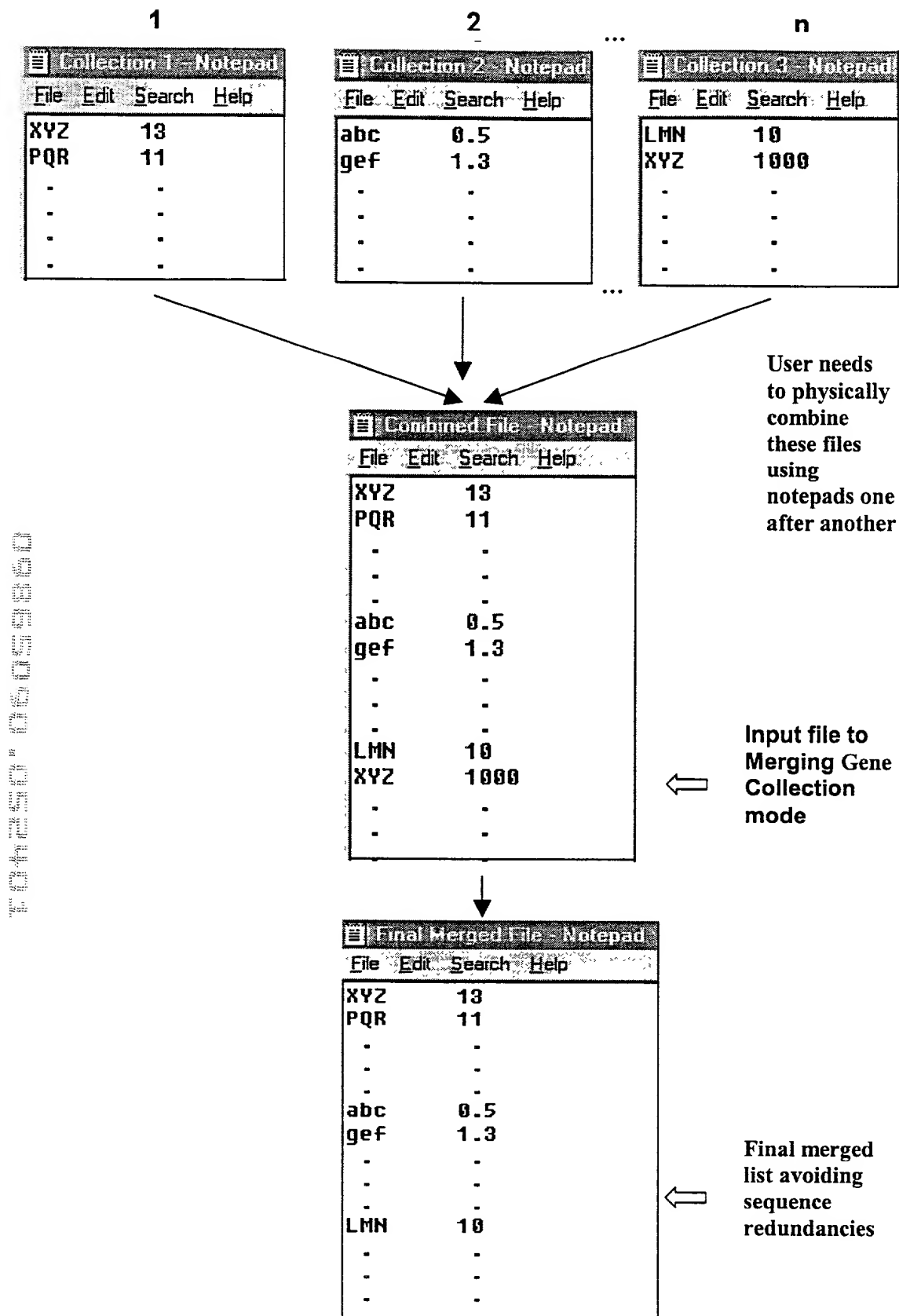


Fig 24

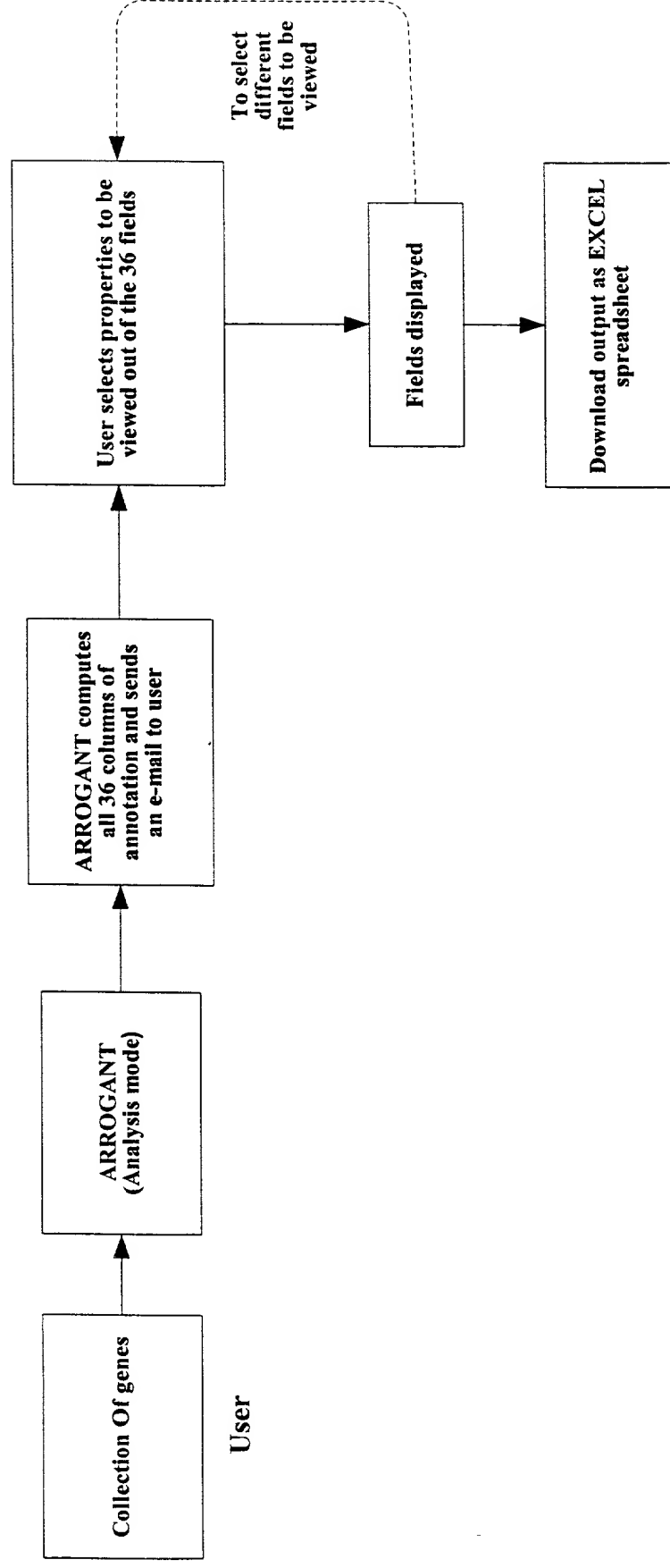


Fig 25

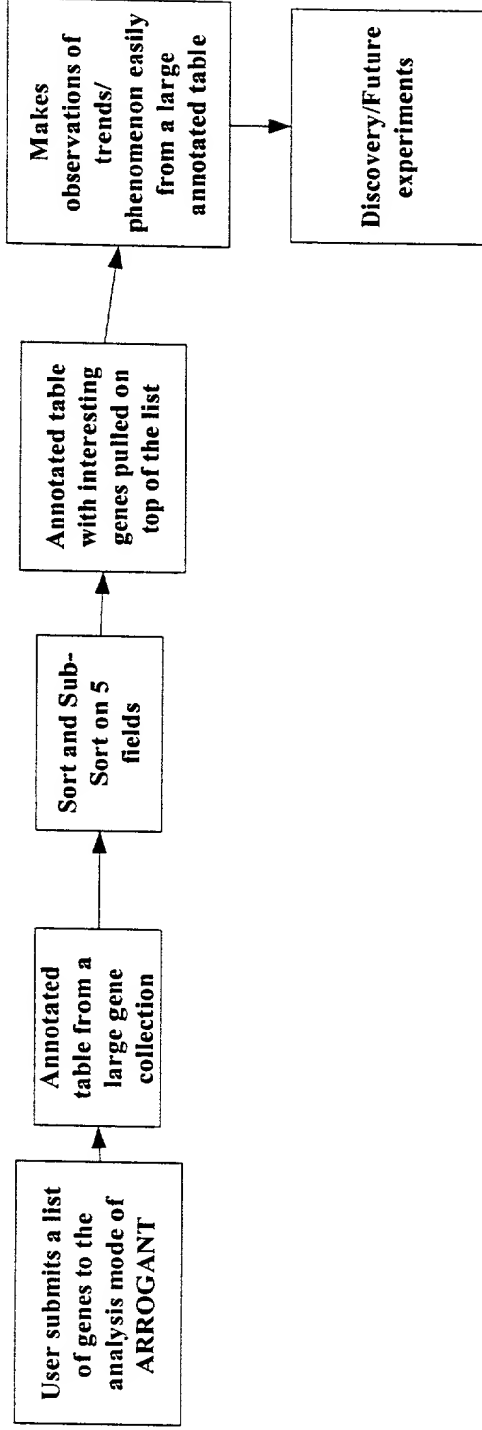


Fig 26

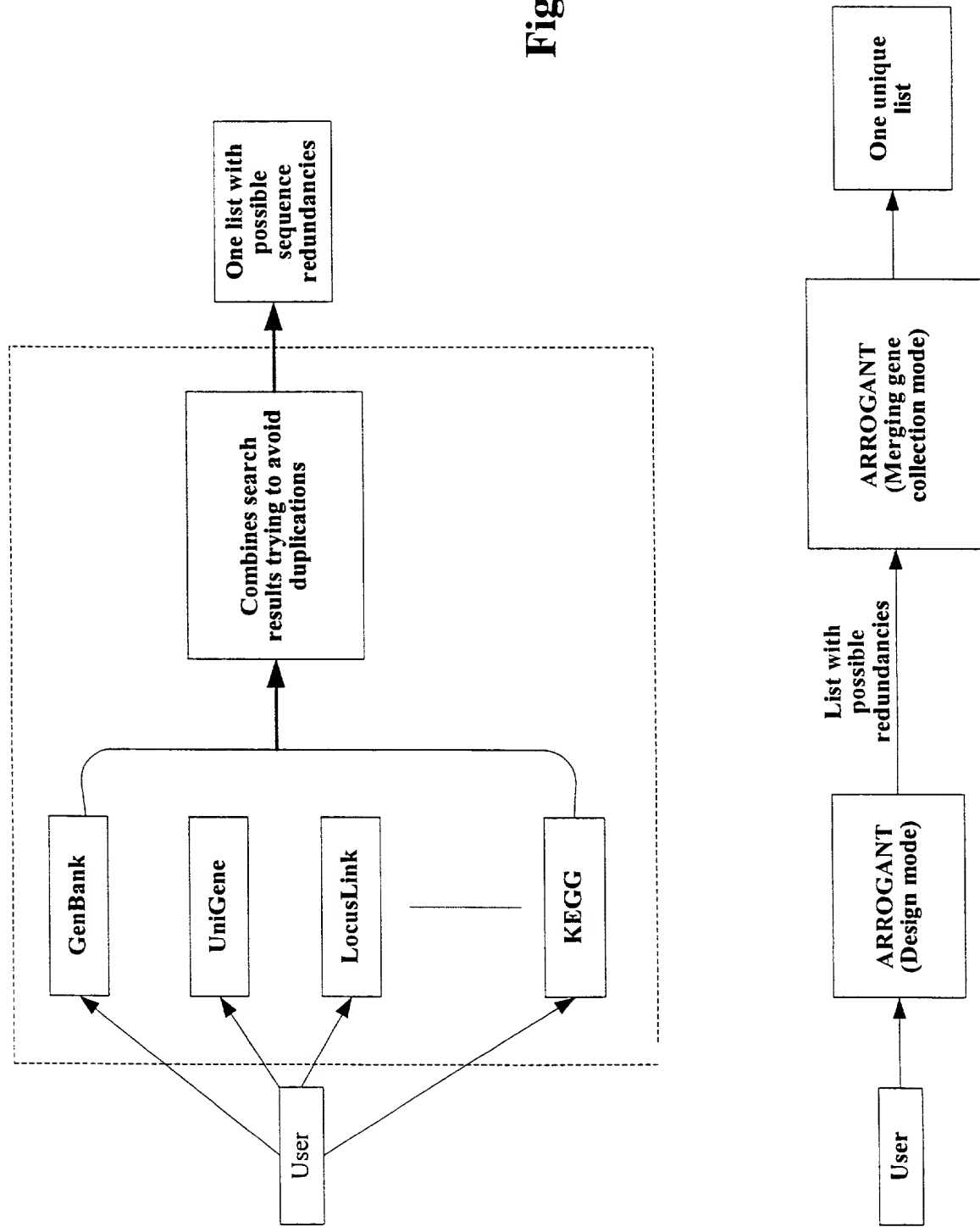


Fig 27

Patent Application No. 02/000,000

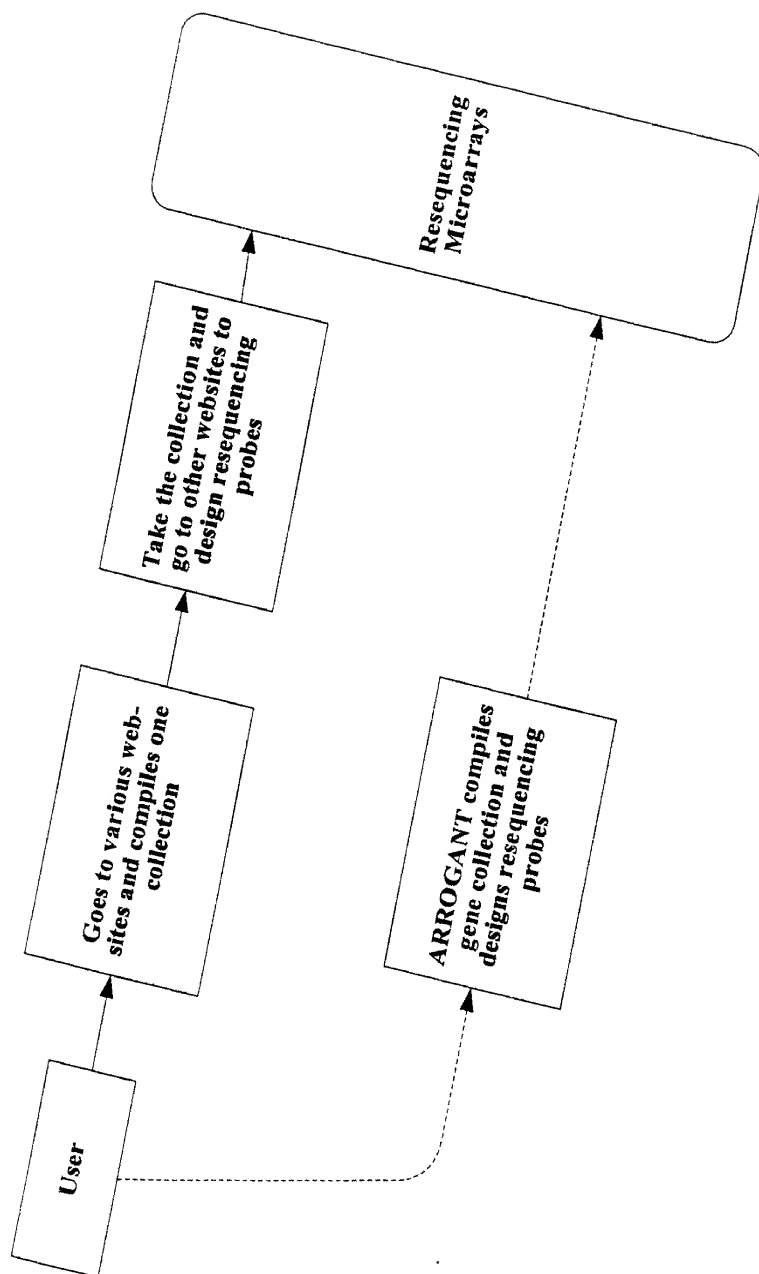


Fig 28

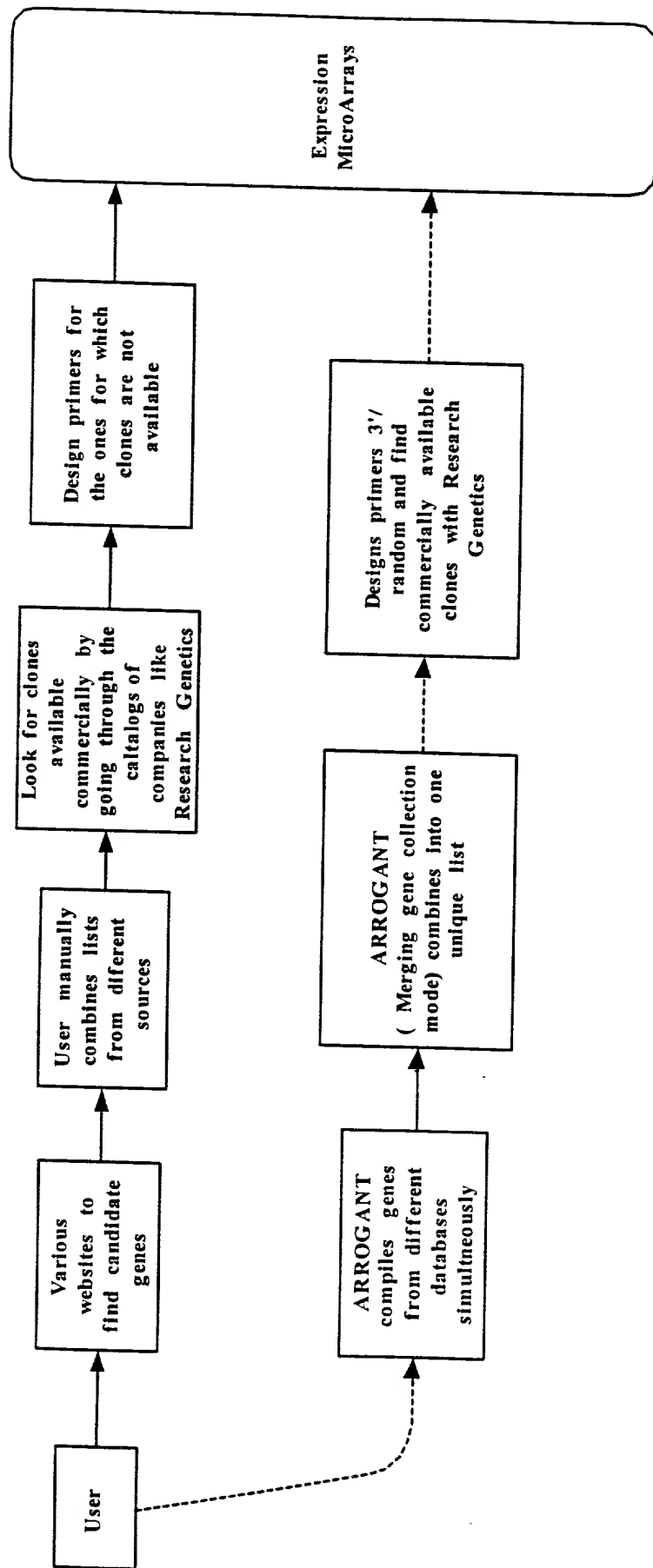


Fig 29

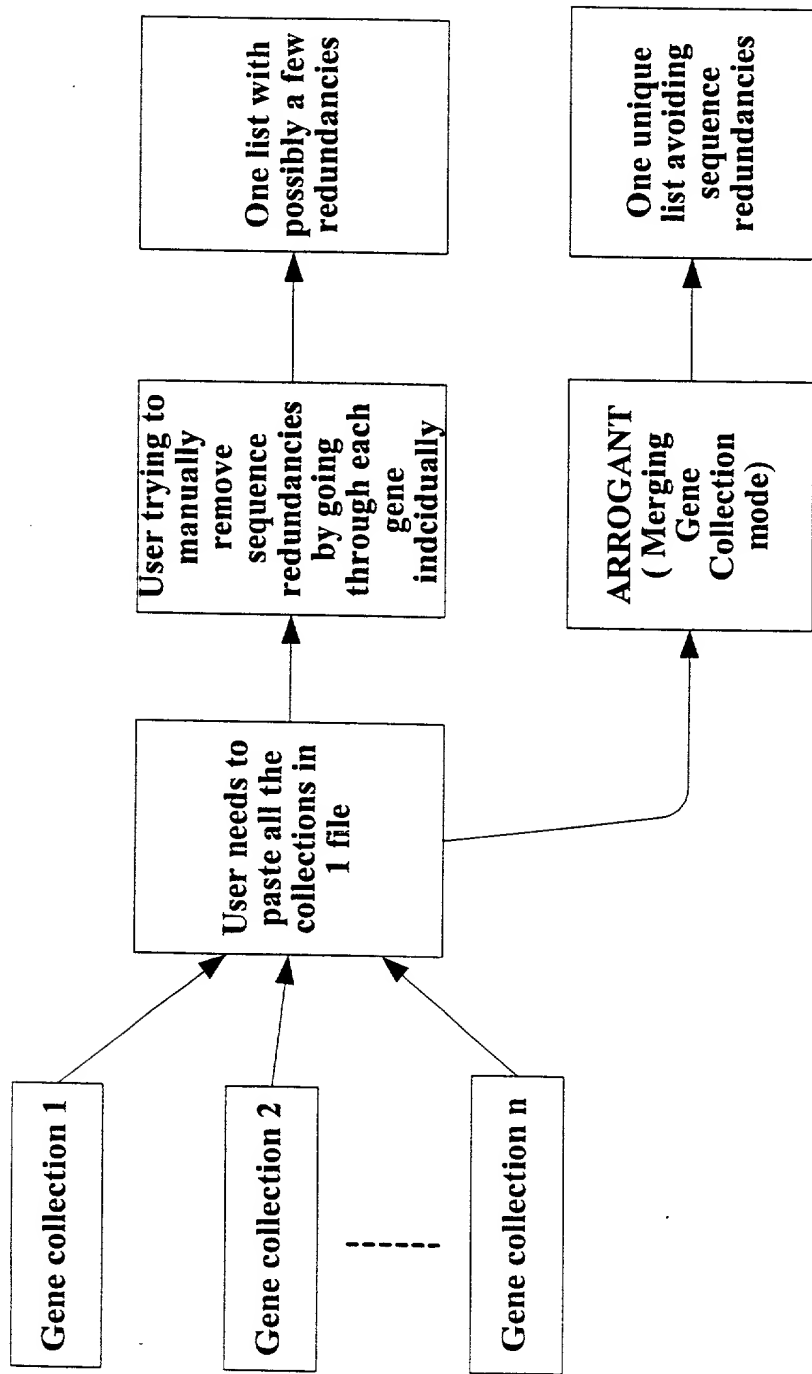


Fig 30

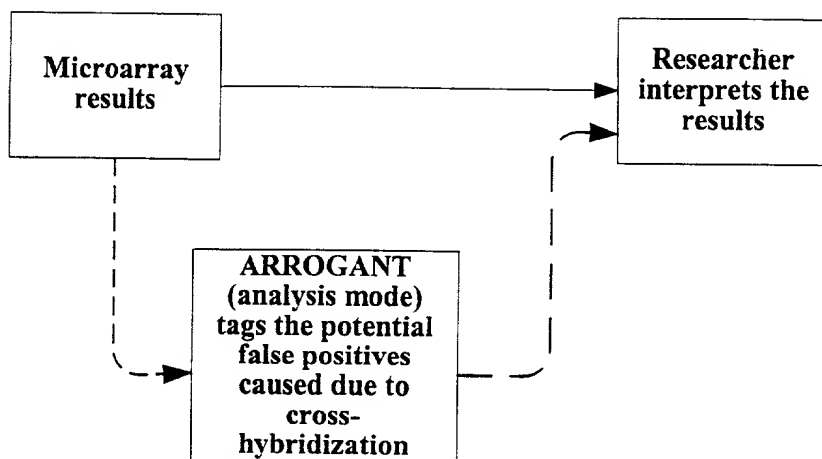


Fig 31a

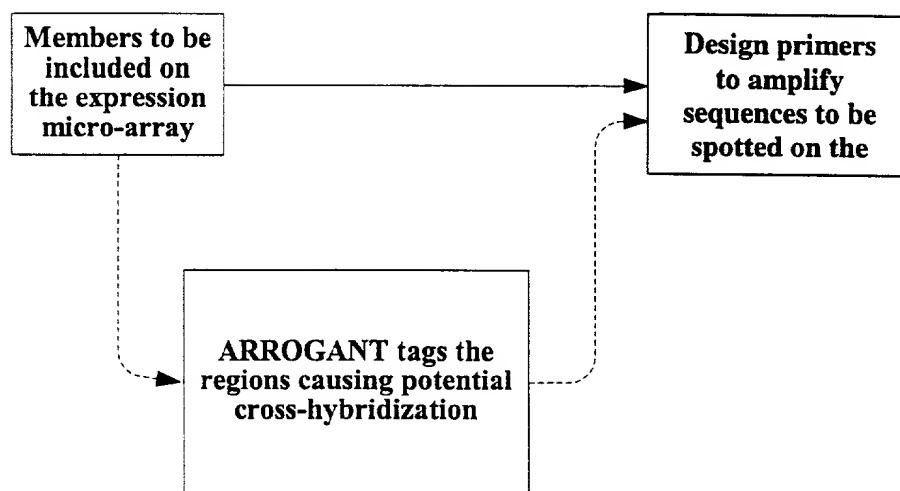


Fig 31b